

GenCore version 5.1.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 16:37:55 : Search time 1361.09 Seconds  
(without alignments)  
15778.007 Million cell updates/sec

Title: US-09-497-967-1  
Perfect score: 1326  
Sequence: 1 atgaataataattttatt.....ttattttttttattttattg 1326

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hci:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hci:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_man:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	404.4	30.5	658	B0135057	B0135057 INIT1_2_G
c 2	389.4	29.4	607	B0134912	B0134912 INIT1_1_F
c 3	367.6	27.7	602	B0135164	B0135164 INIT1_4_B
c 4	366.6	27.6	590	B0135179	B0135179 INIT1_4_C
c 5	317	23.9	502	B0134889	B0134889 INIT1_1_D
c 6	316.6	23.9	675	B0135196	B0135196 INIT1_4_E

c 7	308.2	23.2	445	14	B0134871	B0134871
c 8	294.4	22.2	419	14	B0135036	INIT1_1_B
c 9	280.6	21.2	661	14	B0135189	INIT1_2_D
c 10	263.8	19.9	599	14	B0134821	INIT1_4_D
c 11	249.2	18.8	592	14	B0134985	INIT1_2_G
c 12	240.8	18.2	538	14	B0134810	INIT1_2_D
c 13	237.4	17.9	631	14	B0134827	INIT1_4_C
c 14	236.6	17.8	630	14	B0134905	INIT1_4_E
c 15	227.4	17.1	687	14	B0135168	INIT1_1_F
c 16	205.6	15.5	622	14	B0134798	INIT1_1_E
c 17	202.6	15.4	540	14	B0134798	INIT1_4_B
c 18	202.6	15.3	337	14	B0134748	INIT1_4_B
c 19	196.4	14.8	523	14	B0134970	INIT1_1_C
c 20	179.6	13.5	560	14	B0135129	INIT1_3_E
c 21	144.2	10.9	514	14	B0134761	INIT1_2_D
c 22	99.8	7.5	210	14	B0134900	INIT1_3_F
c 23	86.6	6.5	150	14	B0135114	INIT1_3_E
c 24	72	5.4	978	17	CNS040R1	Tetraodon
c 25	71	5.4	805	17	CNS04RW2	Tetraodon
c 26	70	5.3	747	13	EG918691	AL304427
c 27	67.2	5.1	572	17	CNS043SN	BC918691
c 28	63.8	4.8	938	17	CNS07CG2	602818643
c 29	63.6	4.8	590	17	CNS03M22	AL273200
c 30	61.4	4.6	450	17	FR0025883	AL439128
c 31	61	4.6	711	13	BM588321	T7 end of
c 32	60	4.5	526	17	AZ312601	Tetraodon
c 33	59.2	4.5	773	17	CNS01VTG	AL018519
c 34	59	4.4	935	17	CNS033D4	F.rubripe
c 35	58.8	4.4	536	17	FR0036552	BM588321
c 36	58.8	4.4	927	17	CNS01J4S	170006873
c 37	58.8	4.4	932	17	CNS01G45	AL169549
c 38	58.4	4.4	787	13	BJ282421	Tetraodon
c 39	58.2	4.4	576	9	AA754683	AL124081
c 40	58.2	4.4	735	17	CNS04NSM	Fugu rubr
c 41	58	4.4	947	17	CNS01IS7	AL25985
c 42	57.4	4.3	699	13	BM630395	Tetraodon
c 43	57.4	4.3	1101	17	CNS0039G	AL146136
c 44	57.2	4.3	650	17	AZ573029	Anopheles
c 45	57.2	4.3	1002	17	CNS01N61	BM630395

# ALIGNMENTS

RESULT 1  
B0135057/c  
LOCUS  
DEFINITION  
B0135057 658 bp mRNA linear EST 22-APR-2002  
multifiliis cDNA, mRNA sequence.  
ACCESSION  
B0135057  
VERSION  
B0135057.1 GI:20261156  
KEYWORDS  
EST.  
SOURCE  
Ichthyophthirius multifiliis.  
ORGANISM  
Ichthyophthirius multifiliis.  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Ophryoglenina; Ichthyophthirius.  
REFERENCE  
1 (bases 1 to 658)  
Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,  
Dickerson,H., Lin,T.-L. and Pratt,L.H.  
An EST database for Ichthyophthirius multifiliis (G5 isolate)  
Unpublished (2002)  
JOURNAL  
COMMENT  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Email: mmpratt@uga.edu  
Fax: 706 583 0210

Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.  
Seq primer: T7  
High quality sequence start: 67

1

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|||||
Db 187 GATACATGTACTGAATGTTCTTAAATAAATTAACTTCGTGGTGCTACAGCTAAAGTATATGCT 128
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Qy 1240 GAAGCTACTCAAAAGTATATCGGCTCCACTACTTTCCGCTAAATTTTATCGATTTCC 1299
|||||
Db 127 GAAGCTACTTAAAGACATANTGCGGAGTTCACACTTTCGCAAAATTTTATCAATGTCC 68
|||||
Qy 1300 TTATTATTTATTTCTTTCTTATTTATTG 1326
|||||
Db 67 TTAATATTTATTTCTTTCTTATTGTTG 41
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RESULT 3
BQ135164/c
LOCUS BQ135164 602 bp mRNA linear EST 22-APR-2002
DEFINITION INIT1_4_B05.g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
ACCESSION BQ135164
VERSION BQ135164.1 GI:20261263
KEYWORDS EST.
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 602)
Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: T7
High quality sequence start: 3
High quality sequence stop: 602
POLYA=Yes.

FEATURES
Location/Qualifiers
source 1..602
/organism="Ichthyophthirius multifiliis"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/notes="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 214 a 103 c 92 g 193 t
ORIGIN
|||||

Query Match 27.7%; Score 367.6; DB 14; Length 602;
Best Local Similarity 81.9%; Pred. No. 9.8e-69;
Matches 424; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 809 CAGCTGCCTAAGCTAATTTAGCCACATATGTCAGTACTTAATGTCCACTGGCAGCTGCAA 868
|||||
Db 599 CAGCTCTTGAGGCTAATTTAGCCGCATAATGTGGCCACTGAATGTCCTGCGCACTTTG 540
|||||
Qy 869 TTCAGACGGAGTGACACACTTGTGTTTAGTAATTCATCCACATAATGTTCTTAATGCATTG 928
|||||
Db 539 TTACAGACGGAGTAACACCTACTTATCTATCTATCTATCTCATATGTTATTTGTAAG 480
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Qy 929 CTAATTACTTTTATGTTAATTTTCGACGAGGTAAGTTAATGTTTAAAGTCTCCAG 988
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Db 479 CTGCTTTTACTAAAACTAGTAATTTTCGAAGCAGGTAAAAAGTTAATGCAATAAGTGTGCAG 420
Qy 989 TAAGTAAAACTACTCTCCAGCACATGCTCCAGGTAATAACTGCTACTTAAAGCCACATATGTT 1048
|||||
Db 419 TAAGTAAACTGTTTCCAGCATCTGTTCCAGGTAATAGTCTACTTCCAGCCACATATGTT 360
|||||
Qy 1049 TGACCACATGCTCTGCTGGTACAGTACTTGTGATGGAGACATCAACTAATTTTGTAGCTT 1108
|||||
Db 359 AAAACGATTTGCCCTGCTGGTACAGTGGTTGATGGGTACATCAACTAATTTTGTAGCTT 300
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Qy 1109 CCGCAACTGAATGTACTAATGTTCTGCTGGCTTTTTCGATCCAAACAACTGTTTGA 1168
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Db 299 TACCAAGTGAATGTACTAATGTTAGGCTAACTTTTATGTCATCAAAAACATCTGGTTT 240
|||||
Qy 1169 CAGCAGGTACTGATACATGCTACTGAATGCTACTTAAATAATTAACCTTCTGTCGCCACAGCTA 1228
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Db 239 CAGCAGGTACTGATACATGCTACTGAATGTTCTTAAATAATTAACCTTCTGTCGCCACAGCTA 180
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Qy 1229 AAGTATATGCTGAAGCTACTCAAAAAGTATATGATGGCTCCACTACTTTCGCTAAATTTT 1288
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Db 179 AAGTATATGCTGAAGCTACTTAAAGACATATGATGGCTCCACTTTCGCAAAATTTT 120
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Qy 1289 TATCGATTTCCCTTATTATTATTTCTTCTTATTTATTG 1326
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Db 119 TATCAATGCTCTAATATTTATTTCTTCTTATTTGTTG 82
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RESULT 4
BQ135179/c
LOCUS BQ135179 590 bp mRNA linear EST 22-APR-2002
DEFINITION INIT1_4_C08.g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
ACCESSION BQ135179
VERSION BQ135179.1 GI:20261278
KEYWORDS EST.
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 590)
Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: T7
High quality sequence start: 43
High quality sequence stop: 590
POLYA=No.

FEATURES
Location/Qualifiers
source 1..590
/organism="Ichthyophthirius multifiliis"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/notes="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 207 a 103 c 94 g 186 t
ORIGIN

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source		1. 502		/organism="Ichthyophthirius multifiliis"	
				/strain="G5"	
				/db_xref="taxon:5932"	
				/clone_lib="G5 trophont cDNA (INIT1)"	
				/note="Vector: pBluescript SK(-) from Lambda Zap II; Site_1: EcoRI; Site_2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain. Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda ZAP II. Plasmid DNA for sequencing was prepared by mass excision."	
BASE COUNT		185 a	80 c	70 g	167 t
ORIGIN					
Query Match		23.9%	Score 317;	DB 14;	Length 502;
Best Local Similarity		84.6%	Pred. No. 6.9e-58;		
Matches 356;		Conservative 0;	Mismatches 65;	Indels 0;	Gaps 0;
QY	906	CACATAATGTTCTTAATGCAATGCTAATTAATCTTTTAAATGGTAATTCGAACGAGTAA	965		
DB	500	CTCATAATGTTCTTAATGTAAGCTGGCTTTTACTAAATAGTAATTCGAACGAGTAA	441		
QY	966	AGTTAATGTTTAAAGTGTCCAGTAAGTAAACTACTCCAGCATCTCCAGGTAATAC	1025		
DB	440	AAATTAATGCAATAAGTGTGAGTAAGTAAACTGGTTCAGCATCTGTTCCAGTAATAG	381		
QY	1026	TGCTACTTAAAGCCACATAATGTTTGACCACATGTCCTGCTGGTACAGTACTTGTATGATGG	1085		
DB	380	TGCTACTTCAGCCACATAATGTTTAAACGATGGCTGCTGTCAGTGGTGTATGATGG	321		
QY	1086	ACATCAACTAATTTTGTAGCTTCGCAACTCAATGTACTAAATGTTCTGCTGGCTTTT	1145		
DB	320	TACATCAACTAATTTTGTAGCTTTAGCAAGTGAATGTACTAAATGTTAGGCTAACTTTTA	261		
QY	1146	TGCATCAAAACAACTGGTTTACAGCAGGTAATGATCATCTACTCAATGTAATAAAA	1205		
DB	260	TGCATCAAAACAACTGGTTTTCAGCAGGTAATGATCATCTACTCAATGTAATAAAA	201		
QY	1206	ATTAACCTCTGGTGCACAGCTAAAGTATATGCTGAAGTACTCAAAAGTATAATGCGC	1265		
DB	200	ATTAACCTCTGGTGCACAGCTAAAGTATATGCTGAAGTACTCAAAAGTATAATGCGC	141		
QY	1266	CTCCACTACTTTCGGTAAATTTTATCGAATTTCTTATTTATTTCTTCTTATTTATTT	1325		
DB	140	CAGTTCACCTTTGCGAAAATTTTATCAATGCTCCTTAATATTTATTTCTTCTTATTTGTT	81		
QY	1326	G 1326			
DB	80	G 80			
RESULT 6					
BQ135196/c					
LOCUS					
DEFINITION		INIT1_4_E06.g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis cDNA, mRNA sequence.			
ACCESSION		BQ135196			
VERSION		BQ135196.1			
KEYWORDS		EST.			
SOURCE		GI:20261295			
ORGANISM		Ichthyophthirius multifiliis.			
REFERENCE		1 (bases 1 to 675)			
AUTHORS		Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A., Dickerson,H., Lin,T.-L. and Pratt,L.H.			
TITLE		An EST database for Ichthyophthirius multifiliis (G5 isolate)			
JOURNAL		Unpublished (2002)			
COMMENT		Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mmpratt@uga.edu Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20. Seq primer: JEN REV High quality sequence stop: 474 POLYA=Yes. Location/Qualifiers			

Query Match		27.6%	Score 366.6;	DB 14;	Length 590;
Best Local Similarity		81.8%	Pred. No. 1.6e-68;		
Matches 423;		Conservative 0;	Mismatches 94;	Indels 0;	Gaps 0;
QY	810	AGGTGCTTAAGCTAATTTAGCCACATAATGAGTACTTAATGTCACACTGGCACTCAAT	869		
DB	590	AGGTCTTGAGGCTAATTTAGCCGATAATGTGGCACTGAATGCTGCTGGCACTCTTGT	531		
QY	870	TCAACAGGAGTGACACTGTTTTAGTAAATTCATCCACATAATGTTCTTAAATGCAATGC	929		
DB	530	TACAGCGGAGTAACACTCTATTAATGATGATGATGATGATGATGATGATGATGATGATG	471		
QY	930	TAATTAATCTTTTAAATGTAATTTGGAAGGTAATGTTTAAAGTGTCCAGT	989		
DB	470	TGGCTTTTACTAAATAGTAATTTGGAAGGTAATGTTTAAAGTGTGCACT	411		
QY	990	AAATTAATCTCTCAGCACATGTCAGGTAATGCTACTTAAAGCCACATAATGTTT	1049		
DB	410	AAATTAATCTCTCAGCATCTGTTCCAGGTAATGCTACTTCAAGCCACATAATGTTA	351		
QY	1050	GACCCATCTGCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG	1109		
DB	350	AAAGATTCCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG	291		
QY	1110	CGCACTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1169		
DB	290	AGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	231		
QY	1170	ACGAGTCTGATCATCTACTGAATGATGATGATGATGATGATGATGATGATGATGATG	1229		
DB	230	ACGAGTCTGATCATCTACTGAATGATGATGATGATGATGATGATGATGATGATGATG	171		
QY	1230	AGTATGCTGAAGTACTCAAAAGTATAATGCGCTCCACTACTTTCGCTCAATTTT	1289		
DB	170	AGTATGCTGAAGTACTCAAAAGTATAATGCGCTCCACTACTTTCGCTCAATTTT	111		
QY	1290	ATCGATTCCTTATTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1326		
DB	110	ATCAATGCTCTTAAATTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	74		
RESULT 5					
BQ134889/c					
LOCUS					
DEFINITION		INIT1_D07.bl_A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis cDNA, mRNA sequence.			
ACCESSION		BQ134889			
VERSION		BQ134889.1			
KEYWORDS		EST.			
SOURCE		GI:20260988			
ORGANISM		Ichthyophthirius multifiliis.			
REFERENCE		1 (bases 1 to 502)			
AUTHORS		Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A., Dickerson,H., Lin,T.-L. and Pratt,L.H.			
TITLE		An EST database for Ichthyophthirius multifiliis (G5 isolate)			
JOURNAL		Unpublished (2002)			
COMMENT		Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mmpratt@uga.edu Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20. Seq primer: JEN REV High quality sequence stop: 474 POLYA=Yes. Location/Qualifiers			



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QY 1146 TGCATCAAAACAACTGGTTTACAGCAGGTACTGATCATCTACTGAATGTACTAAAA 1205
|||||
Db 204 TGCATCAAAACAACTGGTTTGCAGCAGGTACTGATCATCTACTGAATGTCTAAAA 145
|||||
QY 1206 ATTAACCTCTGGTGCACAGCTAAAGTATATGCTGAAGCTACTCAAAAGTATAATGGC 1265
|||||
Db 144 ATTAACCTTTGGTGCACAGCTAAAGTATATGCTGAAGCTACTTAAAAAGCATATGGC 85
|||||
QY 1266 CTCACACTCTTCGCGTAAATTTTATCGATTCCTTATTTATTTATTTCTTCTATTT 1322
|||||
Db 84 CAGTTCACACTTTCGCAAAATTTTATCAATGTCCTTAATATTATTTCTTCTATTT 28
|||||

RESULT 8
BQ135036/c
LOCUS
DEFINITION
INR1L2_D10.g1_A006 G5 trophont cDNA (INR1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
ACCESSION
BQ135036
VERSION
BQ135036.1 GI:20261135
EST.
Ichthyophthirius multifiliis.
SOURCE
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE
1 (bases 1 to 419)
Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL
Unpublished (2002)
COMMENT
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: T7
High quality sequence start: 306
High quality sequence stop: 419
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1..419
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INR1)"
/notes="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 140 a 74 c 73 g 132 t
ORIGIN
Query Match 22.2%; Score 294.4; DB 14; Length 419;
Best Local Similarity 85.4%; Pred. No. 4.9e-53;
Matches 328; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 943 AATGTAATTTTCGACGAGTAAAGTTAATGTTTAAAGTCCAGTAAGTAAACTACT 1002
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Db 416 AATCGTAATTTTCGACGAGTAAAGCTAATGCAACAGTGTGCGTAAGTAACACTGGT 357
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QY 1003 CCAGCACATGCTCCAGGTAATCTGCTACTTAAAGCCACATATGCTTTGACCACATGCTT 1062
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Db 356 TCAGCATCTGTTCCAGGTAATAGTCTACTTTCAGCCACATATGTTAAACGATTGCGCT 297
|||||
QY 1063 GCTGTACAGTACTTGATGATGGACATCAACTAATTTTGTAGCTTCGCCAATCGAATGT 1122
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Db 296 GCTGGTACAGTGGTGTATGATGGTACATCAACTAATTTTGTAGCTTTAGCAAGTGAATGT 237
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QY 1123 ACTAAATGTTCTGCTGGCTTTTTCATCAAAACAACTGGTTTACAGCAGGTACTGAT 1182
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Db 236 ACTAAATGTTAGGCTAACTTTTATGCATCAAAACATCTGGTTTCGACGAGGTACTGAT 177
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QY 1183 ACATGTACTGAATGACTTAAAAAATAACTTCTGGTGCACAGCTAAAGTATATGCTGAA 1242
|||||
Db 176 CCATGTACTGAATGTTTAAAAAATAACTTCCGGTGTACAGCTAAAGTATACGCGAA 117
|||||
QY 1243 GCTACTCAAAAGTATATGCGCTCCACTACTTTCGCTAAATTTTATCGATTTCTCTTA 1302
|||||
Db 116 GCTACTTAAAAAGCATATGCGCCAGTTCCTACTTTCGCAAAATTTTATCAATGCCCTTA 57
|||||
QY 1303 TATTTATTTCTTCTTATTTATTTG 1326
|||||
Db 56 ATATTATTTCTTCTTATTTGTTG 33
|||||

RESULT 9
BQ135189
LOCUS
DEFINITION
INR1L4_D09.g1_A006 G5 trophont cDNA (INR1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
ACCESSION
BQ135189
VERSION
BQ135189.1 GI:20261288
EST.
Ichthyophthirius multifiliis.
SOURCE
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE
1 (bases 1 to 661)
Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL
Unpublished (2002)
COMMENT
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: T7
High quality sequence start: 34
High quality sequence stop: 661
POLYA=No.

FEATURES
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Location/Qualifiers
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/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INR1)"
/notes="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 197 a 127 c 124 g 213 t
ORIGIN
Query Match 21.2%; Score 280.6; DB 14; Length 661;
Best Local Similarity 66.3%; Pred. No. 4.2e-50;
Matches 437; Conservative 0; Mismatches 189; Indels 33; Gaps 1;

QY 448 GTTTTCTGCTGCTGCTCCGCTGCAGGTTGCTGCGCTTACTAGTTAATGTTACCT 507
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Db 1 GATCTTGCTAATAATCTCTGAAGTTCCTAATGTTCTAGCCCTAATGTTAATGCGTAGCT 60
Qy 508 TGCCAACATAACAAAAGATTCTCCCTGCCACTGCAGTGCCTAAGCTAATTTAGCCACA 567
Db 61 TGCTAAGTAACAAGCTGATTCCTCAATTAAGACAGGTGCTTAGGCTAATTTAGCCACA 120
Qy 568 TAATGTAGCAATTAATGTCTCTACTGGCAGCTGTACTGATGATGGAGTGACACTTGTGTTT 627
Db 121 TAATGTAGCAATTAATGTCTCTACTGGCAGCTGTACTGATGATGGAGTGACACTTGTGTTT 180
Qy 628 AATACATCAGCCACATTAATGTCTCTACTGGCAGCTGTACTGATGATGGAGTGACACTTGTGTTT 687
Db 181 ACTTAATCAATCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Qy 688 CCTTAAGGTGAAGCTCTCGCGGTTTAA----- 714
Db 241 CCTTCAGCTCAGATCTCTGGTAATGGATAATTCACCTCCAGGTTAATGATGCAATTCCT 300
Qy 715 GTTTTCTGCTGTGCTGCGGTGAGGTGTTGCTGCGGTACTAGTTAATGTGACCT 774
Db 301 GATGCTGCTACTGCTGCTTAATCTCTATGTTCTGCGCTTAATAGTAATCGTAGCT 360
Qy 775 TGCCAAATAACAAAAGATTCTCTGCCACTGCAGTGCCTAAGCTAATTTAGCCACA 834
Db 361 TGCAATCAAAAAGACCAATCTTAATCCAGATCAGTCTTGAGGCTAATTTAGCCGCA 420
Qy 835 TAATGAGTACTTAATGCTCAACTGGCAGTGCCTAATTCAGACGAGTGACACTTGTGTTT 894
Db 421 TAATGAGTACTTAATGCTCAACTGGCAGTGCCTAATTCAGACGAGTGACACTTGTGTTT 894
Qy 895 AGTAATTCATCCACATAATGCTCTTAATGATGATGATGATGATGATGATGATGATGATGAT 954
Db 481 ACTGATCCTCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Qy 955 GAAGCAGGTAAGATTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1014
Db 541 GAAGCAGGTAAGATTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 600
Qy 1015 CCAGGTAATGCTCTACTTAAGCCACATAATGTTGACACATGCTGCTGCTGCTGCTGCTGCT 1073
Db 601 CCAGGTAATGCTCTACTTAAGCCACATAATGTTGACACATGCTGCTGCTGCTGCTGCTGCT 659

RESULT 10
B0134821/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

B0134821.1 599 bp mRNA linear EST 22-APR-2002
INIT1_4_D09.b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
B0134821
EST
Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 599)
Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 506
POLYA=No.
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/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 191 a 113 c 111 g 183 t 1 others
ORIGIN
Query Match 19.9%; Score 263.8; DB 14; Length 599;
Best Local Similarity 71.6%; Pred. No. 1.7e-46;
Matches 346; Conservative 0; Mismatches 137; Indels 0; Gaps 0;
Qy 675 TAATGCTGTTCTCTTAAGGTGAAGCTCCTGGCGTTAAGTTTAAAGTTTGTGCTGGTGC 734
Db 494 TAATGATAAATTCACCTCCAGGTTAATGATGCAAACTCTGATGCTGCTACTGCTGCTTA 435
Qy 735 CGCTGCAGGTGTTGCTGCGTTACTAGTTAATGTTACTTCCCAATAAACAACAAACGA 794
Db 434 AATTCCTATGTTCTGCGCCCTAATAGTAATGCGTAGCTTCCGAATCAAAAAGACCAA 375
Qy 795 TTCTCTGCGACTGCGAGTGCCTAAGCTAAATTTAGCCACATAATGCAGTACTTAATGTCC 854
Db 374 TTCTTAATCCAGATCAGGTCTTGAGGCTAATTTAGCCGCATATAGTGGCACTGAATGTCC 315
Qy 855 AACTGGCACTGCAATTCAGACGGAGTGACACTGTTTTTAAAGTAAATGCACATAATG 914
Db 314 TGCTGGCACTCTGTTACAGACGGAGTAACACCTACTTATATCTGATCTACTCATAATG 255
Qy 915 TTCTTAATGCAATGCTAATTTACTTTTAAATGGTAATTTTCGAAGCAGGTAAGTTAATG 974
Db 254 TGTTAATTTGAAGCTGGCTTTTACTAATAGTAATTTTCGAAGCAGGTAAGTTAATG 195
Qy 975 TTTAAGTGTCCAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 1034
Db 194 CAATAAGTGTGAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 135
Qy 1035 AGCCACATAATGTTGACCAATGCTCCTGCTGGTACAGTACTTGTATGATGAGAACATCAAC 1094
Db 134 AGCCACATAATGTTGACCAATGCTCCTGCTGGTACAGTACTTGTATGATGAGAACATCAAC 75
Qy 1095 TAATTTTGTAGCTTCCGCAACTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1154
Db 74 TAATTTTGTAGCTTCCGCAACTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 15
Qy 1155 AAC 1157
Db 14 AAC 12

RESULT 11
B0134985
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

B0134985
INIT1_2_G01.b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
B0134985
EST
Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 592)
Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
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Db 386 CAATAAGTGTGACAGTAAGTAACTGTTCCAGCATCTGTTCCAGTAATAGTGTCTACTTC 445
QY 1035 AGCCACATAATGTTGACACATGTCCTGCTGTACAGTACTGTGATGGAACATCAAC 1094
Db 446 AGCCACATAATGTTAAACAGGATTCGCCCTGCTGTGATGAGTGGTGTATGATGATCAAC 505
QY 1095 TAATTTTGTAGCTTCGCCCACTCAATGTACTA 1126
Db 506 TAATTTTGTAGCTTTAGCAAGTGAATGTACTA 537

RESULT 13
BQ134827
LOCUS BQ134827 631 bp mRNA linear EST 22-APR-2002
DEFINITION IN17L4_E06.bl.A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
ACCESSION BQ134827
VERSION BQ134827.1 GI:20260926
KEYWORDS EST.
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis.
REFERENCE Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
AUTHORS Hymenostomatida; Ophryoglenina; Ichthyophthirius.
TITLE Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
JOURNAL Dickerson, H., Lin, T.-L. and Pratt, L.H.
COMMENT An EST database for Ichthyophthirius multifiliis (G5 isolate)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 630
POLYA-No. Location/Qualifiers
1. .630
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/notes="Vector: pBluescript SK(-) from Lambda zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda zap
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 180 a 120 c 118 g 213 t
ORIGIN

Query Match 17.9% Score 237.4; DB 14; Length 631;
Best Local Similarity 65.8% Pred. No. 7.6e-41;
Matches 415; Conservative 0; Mismatches 171; Indels 45; Gaps 3;

QY 6 ATATAAATATTTTAAATTTTAAATTTTCTTTTATTTATTAATGAATTAAGAGCTGTCC 65
Db 12 ATTTAATATTTTAAATAATTTTGAATTTTCTTTATTTATTAATGAATTAAGAGCTGTAA 71
QY 66 ATGTCCTGATGCTACTTAGACTCAAGCTGGATTCAGTGTAGTGGCTGCTGCTGATCTGG 125
Db 72 TTGTCCTAAGGCTGCTGCAATTCGGAATTCGGAATTAATCTGATACAGAGCTGCAGATATAA 131
QY 126 TACTGTGTAAATTCAGACACTAATTTTACTATATGTTGGTGGCTGCTTAAGGAGAACC 185
Db 132 TACTTGTACTCATGTGCTAAACACACTTTTACTTTAATGTTGGTAACTTCGTCAGGTCAGGC 191

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QY 186 TAATGGTAATTAACCTTTTCGACAGAAATAATAGTCTAGAGGTATATGTGTACCATGCCA 245
Db 192 TCCTGGTGTGTACAAATTC-----AATCCAGTGTGTAGTCAGTGCATAGCTTGCCA 242
QY 246 AATAACAGAGTAGGCTCTGTTTACCAGTGCAGGTGACTTGTAGTACTTTTAGCCACATAATG 305
Db 243 AGTACACAAAGCGGATTTCTCAACACAGATAAGGTGGTGATGCTAATTTAGCCGCAATAATG 302
QY 306 CAGTACTTAATGTCCTTACTGGCAGTGCATTCGATGATGGAGTGACAGATGTTTTTGATAG 365
Db 303 TAGCAACTTATGTCCTGCTGGCAGTGCAGTTGAAGATGGA---TCACCTACTTTTACTTA 359
QY 366 ATCAGCGGCATAATGTGTTAAATGCAAACTAACTTTTACTATAATGGTGGTTCCTCCTTA 425
Db 360 ATCCCTCACATAATGTGTTAAATGTTAAACCTAACTTTTACTTTAATGGTGTAACTCTAC 419
QY 426 AGGTGAAGCTCTGGCGGTTAA-----GTTTTT 452
Db 420 AGGTGAGGCTCTGGTGGGATAATTCGATCCAACTTAATTTGATTCGAAATCCCTGATCT 479
QY 453 TGCTGTGCTGTGCTGCGCTGCAGGTGTTGCTGCCGTGTACTAGTTAATGTGACCTTGCCA 512
Db 480 TGTATAATCTCGAGTTCCTAATGTTTCTAGCCCTAATGGTTAATCGGTAGCTTGCTA 539
QY 513 ACTAAACAAAACGATTCCTGCCACTGCAGGTGCCTAAGCTAATTTAGCCACATAATG 572
Db 540 AGTAAACAAGTCTGATCTCTCAATTAAGACCAGGTGCTTAGCTAATTTAGCCACATAATG 599
QY 573 TAGCAATTAATGCTCTACTGCGCAGTGTACTT 603
Db 600 TAACAATGAATGCTCTACTGCGCAGTGTACTT 630

RESULT 14
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LOCUS BQ134905 630 bp mRNA linear EST 22-APR-2002
DEFINITION IN17L1_F04.bl.A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
ACCESSION BQ134905
VERSION BQ134905.1 GI:20261004
KEYWORDS EST.
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis.
REFERENCE Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
AUTHORS Hymenostomatida; Ophryoglenina; Ichthyophthirius.
TITLE Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
JOURNAL Dickerson, H., Lin, T.-L. and Pratt, L.H.
COMMENT An EST database for Ichthyophthirius multifiliis (G5 isolate)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 629
POLYA-No. Location/Qualifiers
1. .630
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/notes="Vector: pBluescript SK(-) from Lambda zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.

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Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda ZAP II plasmid DNA for sequencing was prepared by mass

BASE COUNT	179	a	120	c	118	g	213	t
ORIGIN								
Query Match	17.8%; Score 236.6; DB 14; Length 630;							
Best Local Similarity	65.5%; Pred. No. 1.1e-40;							
Matches 416; Conservative	0; Mismatches 174; Indels 45; Gaps 3;							
Qy	2	TGAAATATAATATTTTATTAAATTTTAATTAATTCCTTATTAATGAATTAAGAGCTG	61					
Db	7	TGTCGTTAATATTTTAATAATTTTGATATATTCCTTATTAATGAATTAAGAGCTG	66					
Qy	62	TTCCATGCTCGATGGTACTTAGACTCAAGCTGGATTGACGTAGGTAGTGCCTGATC	121					
Db	67	TTAATTGCTCAATGGTGTGCAATTGCCAATGGNATACTGATACAGGAGCTGCAGATA	126					
Qy	122	TTGTACTTGTGTTAATTCAGACACCTAATTTTACTATAATGGTGGTGCCTTTAGGAG	181					
Db	127	TAAATACTTGTACTCATTCGTA AAAACA CT TT TACTTTAATGGTGGTAATCCTCGAGGTC	186					
Qy	182	AAGCTAATGGTAATTAACCTTTTCGACAGCAATAAGTCTGTAGAGTATATGTTACCAT	241					
Db	187	AGGCTCTGTGCTGTACAATTC-----AATCCAGGTGTTAGTACGTGCATAGCTT	237					
Qy	242	GCCAAATAAACAGAGTAGGCTCTGTACC AATGCAGGTGACTTTAGCTACTTTTAGCCACAT	301					
Db	238	GCCAAGTACAAAGCCGATTCACACACAGATAGGTGGTGATCTAAATTTAGCCGCAT	297					
Qy	302	AATGCAGTACTTAAATGTCCTACTGGCACATGCCTTGATGATGGAGTGACAGATGTTTTG	361					
Db	298	AATGTAGCAACTTATGTCCTGTCTGGCACATGCAGTTTGAAGATGGA---TCACCTACTTTTA	354					
Qy	362	ATAGATCAGCCGATATATGTTTAAATGCACAACTTAACCTTTTACTATAATGGTGGTCTC	421					
Db	355	CCTAATCCCCTACATAATGTTAATGTGTAATGTGAACCTTAACCTTTTACTTAA TG TGGTAA TC	414					
Qy	422	CTTAAGGTGAAGCTCCCTGGCGTTTAA-----G	448					
Db	415	CTACAGGTCAGGCTCCCTGGTGTGGATAAATCGATCCAACTTAATTGATTCGAATCCTG	474					
Qy	449	TTTTTGTGCTGTGCTGCCGCTGCAGGTGTTGCTCCGCTTACTAGTTAATGTGCTACT	508					
Db	475	ATCTTGTCTAATTAATCCCTGAAGTTCCCTAAATGTTTCTAGCCCTAATGGTTAATGCGTAGCTT	534					
Qy	509	GCCAACTAAACAAAAAGATTTCCCTGCCACTGCAGGTGCCTTAAGCTAATTTAGCCACAT	568					
Db	535	GCTAAGTAAACAGCTCGATTCCTCAATTAGACCAGGTGCTTAGGCTAATTTAGCCACAT	594					
Qy	569	AATGTAGCAATTAATGTCTCTACTGGCAGCTGACTT	603					
Db	595	AATGTAAACAATGAATGCTCTACTGGCACTGCTATT	629					

RESULT 15	BQ135168	687 bp	mRNA	linear	EST 22-APR-2002
LOCUS	BQ135168				
DEFINITION	INIT1_4_B09.g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis cDNA, mRNA sequence.				
ACCESSION	BQ135168				
VERSION	BQ135168.1	GI:20261267			
KEYWORDS	EST.				
SOURCE	Ichthyophthirius multifiliis.				
ORGANISM	Ichthyophthirius multifiliis				
	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;				
	Hymenostomatida; Ophryoglenina; Ichthyophthirius.				
REFERENCE	1 (bases 1 to 687)				
AUTHORS	Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A., Dickerson, H., Lin, T.-L. and Pratt, L.H.				
TITLE	An EST database for Ichthyophthirius multifiliis (G5 isolate)				
JOURNAL	Unpublished (2002)				

Search completed: February 16, 2003, 22:24:44  
Job time : 1372.09 secs

